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1600

RAW SEQUENCE LISTING

DATE: 06/12/2003

PATENT APPLICATION: US/09/965,640A

TIME: 14:30:48

Input Set : A:\0315-C revised 6-4-03.txt

Output Set: N:\CRF4\06122003\I965640A.raw

3 <110> APPLICANT: Sims, John E.
5 <120> TITLE OF INVENTION: IL-1 DELTA DNA AND POLYPEPTIDES
7 <130> FILE REFERENCE: 0315-C
9 <140> CURRENT APPLICATION NUMBER: 09/965,640A
10 <141> CURRENT FILING DATE: 2001-09-27
12 <150> PRIOR APPLICATION NUMBER: 09/612,921
13 <151> PRIOR FILING DATE: 2000-07-10
15 <150> PRIOR APPLICATION NUMBER: 60/071,074
16 <151> PRIOR FILING DATE: 1998-01-09
18 <150> PRIOR APPLICATION NUMBER: 60/087,393
19 <151> PRIOR FILING DATE: 1998-06-01
21 <160> NUMBER OF SEQ ID NOS: 11
23 <170> SOFTWARE: PatentIn version 3.2
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 468
27 <212> TYPE: DNA
28 <213> ORGANISM: Mus musculus
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(468)
35 <400> SEQUENCE: 1
36 atg atg gtt ctg agt ggg gca cta tgc ttc cga atg aag gat tca gcc 48
37 Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala
38 1 5 10 15
40 ttg aag gta ctg tat ctg cac aat aac cag ctg ctg gct gga gga ctg 96
41 Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu
42 20 25 30
44 cac gca gag aag gtc att aaa ggt gag gag atc agt gtt gtc cca aat 144
45 His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn
46 35 40 45
48 cgg gca ctg gat gcc agt ctg tcc cct gtc atc ctg ggc gtt caa gga 192
49 Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly
50 50 55 60
52 gga agc cag tgc cta tct tgt ggg aca gag aaa ggg cca att ctg aaa 240
53 Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys
54 65 70 75 80
56 ctt gag cca gtg aac atc atg gag ctc tac ctc ggg gcc aag gaa tca 288
57 Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser
58 85 90 95
60 aag agc ttc acc ttc tac cgg cgg gat atg ggt ctt acc tcc agc ttc 336
61 Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe
62 100 105 110
64 gaa tcc gct gcc tac cca ggc tgg ttc ctc tgc acc tca ccg gaa gct 384

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65 Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala
66      115      120      125
68 gac cag cct gtc agg ctc act cag atc cct gag gac ccc gcc tgg gat      432
69 Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp
70      130      135      140
72 gct ccc atc aca gac ttc tac ttt cag cag tgt gac      468
73 Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
74 145      150      155
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 156
79 <212> TYPE: PRT
80 <213> ORGANISM: Mus musculus
82 <400> SEQUENCE: 2
84 Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala
85 1      5      10      15
88 Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu
89      20      25      30
92 His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn
93      35      40      45
96 Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly
97      50      55      60
100 Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys
101 65      70      75      80
104 Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser
105      85      90      95
108 Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe
109      100      105      110
112 Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala
113      115      120      125
116 Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp
117      130      135      140
120 Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
121 145      150      155
124 <210> SEQ ID NO: 3
125 <211> LENGTH: 468
126 <212> TYPE: DNA
127 <213> ORGANISM: Homo sapiens.
130 <220> FEATURE:
131 <221> NAME/KEY: CDS
132 <222> LOCATION: (1)..(468)
134 <400> SEQUENCE: 3
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136 Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu
137 1      5      10      15
139 aag gtg ctt tat ctg cat aat aac cag ctt cta gct gga ggg ctg cat      96
140 Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
141      20      25      30
143 gca ggg aag gtc att aaa ggt gaa gag atc agc gtg gtc ccc aat cgg      144
144 Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg

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145          35          40          45
147 tgg ctg gat gcc agc ctg tcc ccc gtc atc ctg ggt gtc cag ggt gga      192
148 Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
149          50          55          60
151 agc cag tgc ctg tca tgt ggg gtg ggg cag gag ccg act cta aca cta      240
152 Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
153 65          70          75          80
155 gag cca gtg aac atc atg gag ctc tat ctt ggt gcc aag gaa tcc aag      288
156 Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
157          85          90          95
159 agc ttc acc ttc tac cgg cgg gac atg ggg ctc acc tcc agc ttc gag      336
160 Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
161          100          105          110
163 tcg gct gcc tac ccg ggc tgg ttc ctg tgc acg gtg cct gaa gcc gat      384
164 Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
165          115          120          125
167 cag cct gtc aga ctc acc cag ctt ccc gag aat ggt ggc tgg aat gcc      432
168 Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala
169          130          135          140
171 ccc atc aca gac ttc tac ttc cag cag tgt gac tag      468
172 Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
173 145          150          155
176 <210> SEQ ID NO: 4
177 <211> LENGTH: 155
178 <212> TYPE: PRT
179 <213> ORGANISM: Homo sapiens
181 <400> SEQUENCE: 4
183 Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu
184 1          5          10          15
187 Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
188          20          25          30
191 Ala Gly Lys Val Ile Lys Gly Glu Ile Ser Val Val Pro Asn Arg
192          35          40          45
195 Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
196          50          55          60
199 Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
200 65          70          75          80
203 Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
204          85          90          95
207 Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
208          100          105          110
211 Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
212          115          120          125
215 Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala
216          130          135          140
219 Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
220 145          150          155
223 <210> SEQ ID NO: 5
224 <211> LENGTH: 27

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225 <212> TYPE: PRT
226 <213> ORGANISM: Homo sapiens
228 <400> SEQUENCE: 5
230 Pro Asp Val Ala Ser Leu Arg Gln Gln Val Glu Ala Leu Gln Gly Gln
231 1          5          10          15
234 Val Gln His Leu Gln Ala Ala Phe Ser Gln Tyr
235          20          25
238 <210> SEQ ID NO: 6
239 <211> LENGTH: 33
240 <212> TYPE: PRT
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: leucine zipper peptide
246 <400> SEQUENCE: 6
248 Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
249 1          5          10          15
252 Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
253          20          25          30
256 Arg
260 <210> SEQ ID NO: 7
261 <211> LENGTH: 8
262 <212> TYPE: PRT
263 <213> ORGANISM: Artificial sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: FLAG peptide
268 <400> SEQUENCE: 7
270 Asp Tyr Lys Asp Asp Asp Asp Lys
271 1          5
274 <210> SEQ ID NO: 8
275 <211> LENGTH: 26
276 <212> TYPE: DNA
277 <213> ORGANISM: primer
279 <400> SEQUENCE: 8
280 gggagtctac accctgtgga gctcaa
283 <210> SEQ ID NO: 9
284 <211> LENGTH: 26
285 <212> TYPE: DNA
286 <213> ORGANISM: artificial sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: primer
291 <400> SEQUENCE: 9
292 ctgctggaag tagaagtctg tgatgg
295 <210> SEQ ID NO: 10
296 <211> LENGTH: 30
297 <212> TYPE: DNA
298 <213> ORGANISM: artificial sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: primer
303 <400> SEQUENCE: 10

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308 <211> LENGTH: 28
309 <212> TYPE: DNA
310 <213> ORGANISM: artificial sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: primer
315 <400> SEQUENCE: 11
316 gcattccagc caccattctc gggaagct 28

VERIFICATION SUMMARY

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